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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/736,968A

DATE: 04/12/2002 P.5

TIME: 14:17:34

Input Set : A:\SUB-6-1-1.APP

Output Set: N:\CRF3\04122002\I736968A.raw

3 <110> APPLICANT: Lu, Peter
 4 Garman, Jonathan David
 5 Candia III, Albert Frederick
 6 Arbor Vita Corporation
 8 <120> TITLE OF INVENTION: CLASP-7 Transmembrane Protein
 10 <130> FILE REFERENCE: 020054-000611US
 12 <140> CURRENT APPLICATION NUMBER: US 09/736,968A
 13 <141> CURRENT FILING DATE: 2000-12-13
 15 <150> PRIOR APPLICATION NUMBER: US 60/160,860
 16 <151> PRIOR FILING DATE: 1999-10-21
 18 <150> PRIOR APPLICATION NUMBER: US 60/162,498
 19 <151> PRIOR FILING DATE: 1999-10-29
 21 <150> PRIOR APPLICATION NUMBER: US 60/170,453
 22 <151> PRIOR FILING DATE: 1999-12-13
 24 <150> PRIOR APPLICATION NUMBER: US 60/176,195
 25 <151> PRIOR FILING DATE: 2000-01-14
 27 <150> PRIOR APPLICATION NUMBER: US 60/182,296
 28 <151> PRIOR FILING DATE: 2000-02-14
 30 <150> PRIOR APPLICATION NUMBER: US 09/547,276
 31 <151> PRIOR FILING DATE: 2000-04-11
 33 <150> PRIOR APPLICATION NUMBER: US 60/196,267
 34 <151> PRIOR FILING DATE: 2000-04-11
 36 <150> PRIOR APPLICATION NUMBER: US 60/196,460
 37 <151> PRIOR FILING DATE: 2000-04-11
 39 <150> PRIOR APPLICATION NUMBER: US 60/196,527
 40 <151> PRIOR FILING DATE: 2000-04-11
 42 <150> PRIOR APPLICATION NUMBER: US 60/196,528
 43 <151> PRIOR FILING DATE: 2000-04-11
 45 <150> PRIOR APPLICATION NUMBER: US 09/687,837
 46 <151> PRIOR FILING DATE: 2000-10-13
 48 <150> PRIOR APPLICATION NUMBER: US 60/240,503
 49 <151> PRIOR FILING DATE: 2000-10-13
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 54 <150> PRIOR APPLICATION NUMBER: US 60/240,539
 55 <151> PRIOR FILING DATE: 2000-10-13
 57 <150> PRIOR APPLICATION NUMBER: US 60/240,543
 58 <151> PRIOR FILING DATE: 2000-10-13
 60 <160> NUMBER OF SEQ ID NOS: 115
 62 <170> SOFTWARE: PatentIn Ver. 2.1
 64 <210> SEQ ID NO: 1
 65 <211> LENGTH: 6372
 66 <212> TYPE: DNA

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TECH CENTER 1600/2900

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Output Set: N:\CRF3\04122002\I736968A.raw

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67 <213> ORGANISM: Homo sapiens
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70 <223> OTHER INFORMATION: full length human CLASP-7 cDNA
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73 <221> NAME/KEY: CDS
74 <222> LOCATION: (13)..(6156)
75 <223> OTHER INFORMATION: human CLASP-7
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82 aac agg acg gtg gcc gca gag gtg cgg aag cag gtg tcc cgg gaa cgc 99
83 Asn Arg Thr Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg
84      15          20          25
86 agt ggc tcc ccc cac tcc agc agg cgc tgc agc agc tcc ctg ggg gtc 147
87 Ser Gly Ser Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val
88      30          35          40          45
90 cca ctg act gaa gtt gtc gag ccc ctg gac ttt gag gat gta ctt ctg 195
91 Pro Leu Thr Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu
92      50          55          60
94 agc cgg cca cca gat gct gag ccc ggg ccc ctc agg gac ctg gta gaa 243
95 Ser Arg Pro Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu
96      65          70          75
98 ttc cca gct gat gac ttg gag ctg ctg ctg cag ccc cgg gaa tgc cgg 291
99 Phe Pro Ala Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg
100      80          85          90
102 acc acg gag ccc ggg atc ccc aag gat gaa aaa ctg gat gcc cag gtg 339
103 Thr Thr Glu Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val
104      95          100          105
106 agg gcc gcg gtg gag atg tat att gag gac tgg gtc att gtc cac aga 387
107 Arg Ala Ala Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg
108      110          115          120          125
110 agg tat cag tac ctg agt gca gca tac agc ccc gtc acc aca gac aca 435
111 Arg Tyr Gln Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr
112      130          135          140
114 cag cgg gag cga cag aag ggc ctc ccc cgc cag gtc ttt gag cag gat 483
115 Gln Arg Glu Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp
116      145          150          155
118 gct tct gga gac gag agg tcc ggc cct gag gac tcg aat gac tcc cgg 531
119 Ala Ser Gly Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg
120      160          165          170
122 cgt ggc tcg ggc tcc ccg gaa gac acc cct cga agc agt ggt gcc tct 579
123 Arg Gly Ser Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser
124      175          180          185
126 agc atc ttc gac ctg agg aac ctg gca gct gac tca ttg ctg ccc tct 627
127 Ser Ile Phe Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser
128      190          195          200          205
130 ctg cta gag cgg gcg gcc cca gaa gat gtg gac cgg cgc aat gaa acc 675
131 Leu Leu Glu Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr

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132		210		215		220		
134	ctt cga cgg cag cac cgg ccc ccg gcc ctg ctc acc ctc tac ccg gca	723						
135	Leu Arg Arg Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala							
136		225		230		235		
138	cct gac gag gat gaa gcc gtg gaa cgc tgt agc cgc cca gag cca ccc	771						
139	Pro Asp Glu Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro							
140		240		245		250		
142	cgc gag cac ttt gga caa agg atc ttg gtc aag tgt ctg tcg ctc aag	819						
143	Arg Glu His Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys							
144		255		260		265		
146	ttc gag att gaa att gag ccc atc ttt ggg atc ttg gct ctg tat gat	867						
147	Phe Glu Ile Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp							
148	270		275		280		285	
150	gtg cgg gag aaa aag aag atc tcg gag aac ttc tac ttc gac ctg aac	915						
151	Val Arg Glu Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn							
152		290		295		300		
154	tcg gac tcc atg aag ggg ctg ctt cgg gct cat ggc acc cac cct gcc	963						
155	Ser Asp Ser Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala							
156		305		310		315		
158	atc tcc acc ctg gcc cgc tct gcc atc ttc tct gtg acc tac ccc tca	1011						
159	Ile Ser Thr Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser							
160		320		325		330		
162	cct gac atc ttc ctg gtc atc aag ttg gag aag gtg ctt cag caa ggg	1059						
163	Pro Asp Ile Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly							
164		335		340		345		
166	gac atc agt gag tgc tgt gag cct tac atg gtg ttg aaa gaa gtg gac	1107						
167	Asp Ile Ser Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp							
168	350		355		360		365	
170	aca gcc aag aac aaa gag aag cta gag aag ctg cgc ctg gcg gcc gag	1155						
171	Thr Ala Lys Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu							
172		370		375		380		
174	cag ttc tgc acc cgc ctg ggc cgc tac cgc atg ccc ttc gcc tgg acg	1203						
175	Gln Phe Cys Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr							
176		385		390		395		
178	gcc gtg cac ttg gcc aac atc gtg agc agc gct ggg cag ctg gac cgg	1251						
179	Ala Val His Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg							
180		400		405		410		
182	gac tct gac tcg gag ggc gag cgc cgg cca gcc tgg aca gac cgc cgc	1299						
183	Asp Ser Asp Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg							
184		415		420		425		
186	cgt cgg ggg ccc cag gac cgg gcg agt agt ggg gac gac gcc tgc agc	1347						
187	Arg Arg Gly Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser							
188	430		435		440		445	
190	ttc tct ggc ttc cgt cca gcc acg cta act gtc aca aac ttc ttt aag	1395						
191	Phe Ser Gly Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys							
192		450		455		460		
194	cag gag gct gag cga ctc agt gac gag gac ctc ttc aag ttc ctg gct	1443						
195	Gln Glu Ala Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala							
196		465		470		475		

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198 gac atg agg cgc ccg tcg tcc ctg ctg cgg cga cta cgt cct gtg acI 1491
199 Asp Met Arg Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr
200 480 485 490
202 gcc cag ctc aag atc gac att tct ccg gct cct gaa aat ccc cac ttc 1539
203 Ala Gln Leu Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe
204 495 500 505
206 tgc ctc tcc cct gag ctg ctt cat atc aag ccc tac ccg gac ccc agg 1587
207 Cys Leu Ser Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg
208 510 515 520 525
210 ggc cgg ccc acc aag gag att ctg gag ttc ccc gcc cgc gaa gtc tat 1635
211 Gly Arg Pro Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr
212 530 535 540
214 gcc ccc cat acc agc tac agg aac ctg ctg tac gtg tac ccg cac agc 1683
215 Ala Pro His Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser
216 545 550 555
218 ctc aac ttc agc agc cgc cag ggc tcc gtg cgc aac ctt gct gtg cga 1731
219 Leu Asn Phe Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg
220 560 565 570
222 gtg cag tac atg aca ggc gag gac ccc agc cag gct ctg ccg gtc atc 1779
223 Val Gln Tyr Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile
224 575 580 585
226 ttt ggc aag tcc agc tgc agt gaa ttt acc cgc gag gcc ttc aca ccg 1827
227 Phe Gly Lys Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro
228 590 595 600 605
230 gtg gtc tac cat aac aag tcc ccc gag ttc tac gag gag ttc aag ctg 1875
231 Val Val Tyr His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu
232 610 615 620
234 cat ctt cca gcc tgc gtg aca gag aac cat cac ctg ctg ttc acc ttc 1923
235 His Leu Pro Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe
236 625 630 635
238 tac cat gtc agc tgc cag ccc cgg ccg ggc act gcc ctg gag aca ccc 1971
239 Tyr His Val Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro
240 640 645 650
242 gtg ggc ttt act tgg atc cca ctg ctg cag cac ggg cgc ctg agg acc 2019
243 Val Gly Phe Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr
244 655 660 665
246 ggc ccc ttc tgt ctc cca gtg tct gtg gac cag ccg ccg ccc agc tat 2067
247 Gly Pro Phe Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr
248 670 675 680 685
250 tcc gtg ctc aca ccc gat gtg gcg ctt ccg ggc atg cgc tgg gtg gac 2115
251 Ser Val Leu Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp
252 690 695 700
254 ggt cac aag ggc gtg ttc agt gtg gag ctc aca gcc gtg tcc tct gtg 2163
255 Gly His Lys Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val
256 705 710 715
258 cac ccc cag gac ccc tac ctg gac aaa ttc ttc acc ctg gtg cac gtc 2211
259 His Pro Gln Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val
260 720 725 730
262 ctg gag gag gga gcc ttc cca ttc cgg ctc aag gac act gtg ctg agc 2259

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263	Leu	Glu	Glu	Gly	Ala	Phe	Pro	Phe	Arg	Leu	Lys	Asp	Thr	Val	Leu	Ser	
264		735					740					745					
266	gag	ggc	aac	gtg	gag	cag	gag	ctg	cgg	gcc	agt	ctt	gca	gca	ctg	cgc	2307
267	Glu	Gly	Asn	Val	Glu	Gln	Glu	Leu	Arg	Ala	Ser	Leu	Ala	Ala	Leu	Arg	
268	750					755					760					765	
270	ctg	gcc	agc	ccc	gaa	ccc	ctt	gtg	gcc	ttc	tcc	cac	cac	gtg	ctg	gac	2355
271	Leu	Ala	Ser	Pro	Glu	Pro	Leu	Val	Ala	Phe	Ser	His	His	Val	Leu	Asp	
272					770					775					780		
274	aag	ctc	gtg	cgt	ctg	gtc	atc	agg	ccc	ccg	atc	atc	agt	ggc	cag	att	2403
275	Lys	Leu	Val	Arg	Leu	Val	Ile	Arg	Pro	Pro	Ile	Ile	Ser	Gly	Gln	Ile	
276					785					790					795		
278	gtg	aac	ctg	ggc	cgt	gga	gcc	ttt	gaa	gca	atg	gcc	cat	gta	gtc	agc	2451
279	Val	Asn	Leu	Gly	Arg	Gly	Ala	Phe	Glu	Ala	Met	Ala	His	Val	Val	Ser	
280			800					805					810				
282	ctt	gtt	cac	cgg	agc	ctg	gag	gca	gcc	cag	gat	gcc	cgc	ggt	cac	tgc	2499
283	Leu	Val	His	Arg	Ser	Leu	Glu	Ala	Ala	Gln	Asp	Ala	Arg	Gly	His	Cys	
284			815					820					825				
286	cca	cag	ctg	gct	gcc	tac	gtc	cac	tac	gcc	ttt	cgc	ctt	cct	ggc	act	2547
287	Pro	Gln	Leu	Ala	Ala	Tyr	Val	His	Tyr	Ala	Phe	Arg	Leu	Pro	Gly	Thr	
288	830					835					840					845	
290	gag	ccc	agc	ctc	ccg	gat	ggg	gcc	cct	cca	gtg	aca	gtg	cag	gct	gcc	2595
291	Glu	Pro	Ser	Leu	Pro	Asp	Gly	Ala	Pro	Pro	Val	Thr	Val	Gln	Ala	Ala	
292					850					855					860		
294	aca	ctg	gcc	cgt	ggc	tct	ggt	cgc	ccc	gca	agc	ctc	tac	ctg	gcg	cgt	2643
295	Thr	Leu	Ala	Arg	Gly	Ser	Gly	Arg	Pro	Ala	Ser	Leu	Tyr	Leu	Ala	Arg	
296					865					870					875		
298	tcc	aag	agc	atc	agc	agc	agc	aac	cct	gac	ctc	gcc	gtg	gcc	cct	ggc	2691
299	Ser	Lys	Ser	Ile	Ser	Ser	Ser	Asn	Pro	Asp	Leu	Ala	Val	Ala	Pro	Gly	
300			880					885					890				
302	tct	gtg	gat	gac	gag	gtt	tcc	cgc	atc	ctg	gcc	agc	aag	ctg	ctt	cac	2739
303	Ser	Val	Asp	Asp	Glu	Val	Ser	Arg	Ile	Leu	Ala	Ser	Lys	Leu	Leu	His	
304			895					900					905				
306	gag	gag	ctg	gct	ctg	cag	tgg	gtg	gtc	agc	agc	agt	gcc	gta	cgc	gag	2787
307	Glu	Glu	Leu	Ala	Leu	Gln	Trp	Val	Val	Ser	Ser	Ser	Ala	Val	Arg	Glu	
308	910					915					920					925	
310	gcc	atc	ctc	cag	cac	gcc	tgg	ttc	ttc	ttc	cag	ctc	atg	gtg	aag	agt	2835
311	Ala	Ile	Leu	Gln	His	Ala	Trp	Phe	Phe	Gln	Leu	Met	Val	Lys	Ser		
312					930					935					940		
314	atg	gcg	ctg	cac	ctg	ctg	ctt	ggc	cag	cga	cta	gac	aca	ccc	cgc	aag	2883
315	Met	Ala	Leu	His	Leu	Leu	Leu	Gly	Gln	Arg	Leu	Asp	Thr	Pro	Arg	Lys	
316					945					950					955		
318	ctg	cgc	ttc	ccc	gga	cgc	ttc	ctg	gac	gac	atc	act	gcc	ttg	gtg	ggc	2931
319	Leu	Arg	Phe	Pro	Gly	Arg	Phe	Leu	Asp	Asp	Ile	Thr	Ala	Leu	Val	Gly	
320			960					965					970				
322	tct	gtg	ggc	ctg	gag	gtc	atc	acc	cgt	gtc	cac	aag	gat	gtg	gag	ctg	2979
323	Ser	Val	Gly	Leu	Glu	Val	Ile	Thr	Arg	Val	His	Lys	Asp	Val	Glu	Leu	
324			975					980					985				
326	gcc	gag	cac	ctc	aac	gcc	agc	ctg	gct	ttc	ttc	ctc	agt	gac	ctt	ctg	3027
327	Ala	Glu	His	Leu	Asn	Ala	Ser	Leu	Ala	Phe	Phe	Leu	Ser	Asp	Leu	Leu	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 04/12/2002

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Input Set : A:\SUB-6-1-1.APP

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L:1038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8